In the Specification:

Please amend the specification as shown:

Page 1, before paragraph [0001], please insert the following:

Sequence Listing

The instant application contains a "lengthy" Sequence Listing which has been submitted via CD-R in lieu of a printed paper copy, and is hereby incorporated by reference in its entirety. Said CD-R, recorded on December 4, 2006, are labeled CRF, "Copy 1" and "Copy 2", respectively, and each contains only one identical 892 KB file (28622148.APP).

Please delete the paragraph on page 4, lines 10-33 and replace it with the following paragraph:

It was surprisingly found that the above-recited, specific modifications to known CDR regions as well as framework regions and their corresponding transition sequences lead to deimmunized, CD3 specific binding molecules which show reduced immunogenicity but retain their cytotoxic activity compared to original non-deimmunized sequences. This finding was in particular surprising since not all possible deimmunization protocols led to bioactive, functional constructs which show distinct cytotoxic activity; see appended examples. Furthermore, surprisingly the deimmunized cytotoxically active CD3 binding molecules showed increased productivity. In accordance with this invention, specific sequences of non-deimmunized antibodies have been replaced by/modified to the sequences recited herein above. In particular, in framework H1 regions the original sequence Leu-Ala-Arg (LAR) has been replaced by the sequence Val-Lys-Lys (VKK). Furthermore, the sequence Thr-Ser-Gly-Tyr-Thr-Phe (TSGYTF) **(SEQ ID NO: 410)** comprised in the transition region of framework H1 and CDR-H1 of some non-modified/non-deimmunized CD3specific antibodies has been modified in accordance with the invention to Ala-Ser-Gly-Tyr-Thr-Phe (ASGYTF) (SEQ ID NO.:233) (see Figure 14). A desired, inventive

CD3-specific binding construct is characterized as comprising at least two binding specificities whereby a second binding specificity is Ig-derived. Furthermore, said desired constructs are characterized by the specific amino acid sequences shown herein above. As documented in the appended examples the constructs as provided herein still retain bioactivity in their modified/deimmunized form. The examples also document that not all deimmunizations, determined by methods known in the art (WO 92/10755, WO 00/34317, WO 98/52976, WO 02/079415 or WO 02/012899), lead to bioactive molecules; see in particular the examples 2 and 5.

Please delete the paragraph on page 73, lines 12-21 and replace it with the following paragraph:

Figure 14. Sequence alignment of variable heavy region of the non-deimmunized CD3 antibody **(SEQ ID NO: 110)**, VH5 (SEQ ID NO.:74), VH7 (SEQ ID NO.:76), VH2 (SEQ ID NO.:70) and VH3 (SEQ ID NO.:72). Framework region 1 (FR1), complementarity determining region 1 (CDR1), Framework region 1 (FR1), complementarity determining region 2 (CDR2), Framework region 3 (FR3), complementarity determining region 3 (CDR3) and Framework region 4 (FR4) have been depicted. The sequence LAR and VKK in FR1, the sequence ASGYTF **(SEQ ID NO: 233)** and ASGYTA **(SEQ ID NO: 411)** at the transition of framework 1 region to CDR1 region and the sequence LTTDK **(SEQ ID NO: 412)**, ITTDK **(SEQ ID NO: 235)** and MTTDT **(SEQ ID NO: 413)** at FR3 and the sequence MQLS **(SEQ ID NO: 414)**, MELS **(SEQ ID NO: 234)** and LQMN **(SEQ ID NO: 415)** at FR3 have been boxed. Alignment was carried out using the AlingnX program of Vector NTI Advance (Informax, Inc., USA).

Please delete the paragraph on page 85, lines 4-19 and replace it with the following paragraph:

Example 7. Homology alignment of anti-CD3 (VH5), anti-CD3 (VH7), anti-CD3 (VH2) and anti-CD3 (VH3) with the non-deimmunized anti-CD3 VH

The variable heavy region of the non-deimmunized CD3 antibody, VH5 (SEQ ID NO.:74), VH7 (SEQ ID NO.:76), VH2 (SEQ ID NO.:70) and VH3 (SEQ ID NO.:72) were aligned

using the AlingnX program of Vector NTI Advance (Informax, Inc., USA). The Clustal W algorithm used is described in Nucleic Acid Research, 22 (22): 4673-4860, 1994. The alignment is shown in Figure 14. From the alignment can be seen that the variable regions VH5 and VH7, which show surprisingly good binding have the sequence ASGYTF **(SEQ ID NO: 233)** at the transition region of framework 1 to CDR1. Furthermore, the VH regions showing no binding (VH2 (SEQ ID NO.:70) and VH3 (SEQ ID NO.:72)) comprise the sequence ASGYTA **(SEQ ID NO: 411)** at the transition of framework 1 to CDR1. Thus, for obtaining a construct having reduced propensity to generate T cell epitopes and binding to CD3, the construct has to comprise the sequence ASGYTF **(SEQ ID NO: 233)** at the transition of framework 1 to CDR1. Surprisingly, the variable heavy regions binding to CD3 and showing reduced propensity to generate T cell epitopes comprising the above-mentioned sequence ASGYTF **(SEQ ID NO: 233)** show good binding.